CR[redacted]rror Corrected by the STIC Syst[redacted]Branch

Serial Numb r: 08/779,460B

CRF Processing Date: 4/9/98
Edited by: _____
Verified by: _____ (STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☑ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☑ Deleted extra, invalid, headings used by an applicant, specifically: "TELEAX" - replaced w/ TELEFAX
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ***ending*** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

***Examin r: The abov c rrections must be communicated to th applicant in the first Office Action. DO NOT send a copy of this form.**

3/1/95

This Raw Listing contains the General Information Section and up t the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Oscar Johannes Maria GODDIJN
Teunis Cornelis VERWOERD
Ronny Wilhelmus Hermanus Henrika KRUTWAGEN
Eline VOOGD

(ii) TITLE OF INVENTION: ENHANCED ACCUMULATION OF TREHALOSE IN PLANTS

(iii) NUMBER OF SEQUENCES: 27

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LADAS & PARRY

(B) STREET: 26 WEST 61 STREET

(C) CITY: NEW YORK

(D) STATE: NY

(E) COUNTRY: USA

(F) ZIP: 10023

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3-1/4" Disk 1.44 MB

(B) COMPUTER: IBM PC Compatible

(C) OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11

(D) SOFTWARE: WordPerfect 6.1 for Windows

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/779,460

(B) FILING DATE: 07-JAN-1997

--> 47 (C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PY000009/96

(B) FILING DATE: 12-JAN-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: MASS, Clifford J.

(B) REGISTRATION NO.: 30,086

(C) REF./DOCKET NO.: U-011098-6

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 708-1890

(B) TELEFAX: (212)- 246-8959

(C) TELEX: 233288

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2621 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 25..2485
(D) OTHER INFORMATION: /function= "trehalose phosph.
synthase and trehalose phosph. phosphatase"
/product= "bipartite enzyme"

(ix) FEATURE:
(A) NAME/KEY: unsure
(B) LOCATION: 1609..1611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTGATCCTGC GGTTTCATCA CAAT ATG ATA CTC TTA CAT CTG ATG CCC CTT 51

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100                                 Met Ile Leu Leu His Leu Met Pro Leu
101                                   1               5
102
103  CAG ATG CTC CCA AAT AGG TTG ATT GTC GTA TCG AAT CAG TTA CCC ATA        99
104  Gln Met Leu Pro Asn Arg L u Ile Val Val Ser Asn Gln Leu Pro Ile
105   10                  15                  20                  25
106
107  ATC GCT AGG CTA AGA CTA ACG ACA ATG GAG GGT CCT TTT GGG ATT TCA       147
108  Ile Ala Arg Leu Arg Leu Thr Thr Met Glu Gly Pro Phe Gly Ile Ser
109                 30                  35                  40
110
111  CTT GGG ACG AGA GTT CGA TTT ACA TGC ACA TCA AAG ATG CAT TAC CCG       195
112  Leu Gly Thr Arg Val Arg Phe Thr Cys Thr Ser Lys Met His Tyr Pro
113               45                  50                  55
114
115  CAG CCG TTG AGG TTT TCT ATT CTT GGC GAT CCA CTA AGG GCT GAC GTT       243
116  Gln Pro Leu Arg Phe Ser Ile Leu Gly Asp Pro Leu Arg Ala Asp Val
117           60                  65                  70
118
119  GGC CCT ACC GAA CAA GAT GAC GTG TCA AAG ACA TTG CTC GAT AGG TTT       291
120  Gly Pro Thr Glu Gln Asp Asp Val Ser Lys Thr Leu Leu Asp Arg Phe
121       75                  80                  85
122
123  AAT TGC GTT GCG GTT TTT GTC CCT ACT TCA AAA TGG GAC CAA TAT TAT       339
124  Asn Cys Val Ala Val Phe Val Pro Thr Ser Lys Trp Asp Gln Tyr Tyr
125   90                  95                  100                 105
126
127  CAC TGC TTT TGT AAG CAG TAT TTG TGG CCG ATA TTT CAT TAC AAG GTT       387
128  His Cys Phe Cys Lys Gln Tyr Leu Trp Pro Ile Phe His Tyr Lys Val
129                 110                 115                 120
130
131  CCC GCT TCT GAC GTC AAG AGT GTC CCG AAT AGT CGG GAT TCA TGG AAC       435
132  Pro Ala Ser Asp Val Lys Ser Val Pro Asn Ser Arg Asp Ser Trp Asn
133               125                 130                 135
134
135  GCT TAT GTT CAC GTG AAC AAA GAG TTT TCC CAG AAG GTG ATG GAG GCA       483
136  Ala Tyr Val His Val Asn Lys Glu Phe Ser Gln Lys Val Met Glu Ala
137           140                 145                 150
138
139  GTA ACC AAT CGT AGC AAT TAT GTA TGG ATA CAT GAC TAC CAT TTA ATG       531
140  Val Thr Asn Arg Ser Asn Tyr Val Trp Ile His Asp Tyr His Leu Met
141       155                 160                 165
142
143  ACG CTA CCG ACT TTC TTG AGG CGG GAT TTT TGT CGT TTT AAA ATC GGT       579
144  Thr Leu Pro Thr Phe Leu Arg Arg Asp Phe Cys Arg Phe Lys Ile Gly
145  170                 175                 180                 185
146
147  TTT TTT CTG CAT AGC CCG TTT CCT TCC TCG GAG GTT TAC AAG ACC CTA       627
148  Phe Phe Leu His Ser Pro Phe Pro Ser Ser Glu Val Tyr Lys Thr Leu
149                 190                 195                 200
150
151  CCA ATG AGA AAC GAG CTC TTG AAG GGT CTG TTA AAT GCT GAT CTT ATC       675
152  Pro Met Arg Asn Glu Leu Leu Lys Gly Leu Leu Asn Ala Asp Leu Ile
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153                 205                 210                 215
154
155   GGG TTC CAT ACA TAC GAT TAT GCC CGT CAT TTT CTA ACG TGT TGT AGT       723
156   Gly Ph  His Thr Tyr Asp Tyr Ala Arg His Phe Leu Thr Cys Cys Ser
157           220                 225                 230
158
159   CGA ATG TTT GGT TTG GAT CAT CAG TTG AAA AGG GGG TAC ATT TTC TTG       771
160   Arg Met Phe Gly Leu Asp His Gln Leu Lys Arg Gly Tyr Ile Phe Leu
161       235                 240                 245
162
163   GAA TAT AAT GGA AGG AGC ATT GAG ATC AAG ATA AAG GCG AGC GGG ATT       819
164   Glu Tyr Asn Gly Arg Ser Ile Glu Ile Lys Ile Lys Ala Ser Gly Ile
165   250                 255                 260                 265
166
167   CAT GTT GGT CGA ATG GAG TCG TAC TTG AGT CAG CCC GAT ACA AGA TTA       867
168   His Val Gly Arg Met Glu Ser Tyr Leu Ser Gln Pro Asp Thr Arg Leu
169                 270                 275                 280
170
171   CAA GTT CAA GAA GTC CAA AAA CGT TCG AAG GAA ATC GTG CTA CTG GGA       915
172   Gln Val Gln Glu Val Gln Lys Arg Ser Lys Glu Ile Val Leu Leu Gly
173           285                 290                 295
174
175   GTT GAT GAT TTG GAT ATA TTC AAA GGT GTG AAC TTC AAG GTT TTA GCG       963
176   Val Asp Asp Leu Asp Ile Phe Lys Gly Val Asn Phe Lys Val Leu Ala
177           300                 305                 310
178
179   TTG GAG AAG TTA CTT AAA TCA CAC CCG AGT TGG CAA GGG CGT GTG GAA      1011
180   Leu Glu Lys Leu Leu Lys Ser His Pro Ser Trp Gln Gly Arg Val Glu
181       315                 320                 325
182
183   AAG GTG CAA ATC TTG AAT CCT CTG CGC CGT TGC CAA GAC GTC GAT GAG      1059
184   Lys Val Gln Ile Leu Asn Pro Leu Arg Arg Cys Gln Asp Val Asp Glu
185   330                 335                 340                 345
186
187   ATC AAT GCC GAG ATA AGA ACA GTC TGT GAA AGA ATC AAT AAC GAA CTG      1107
188   Ile Asn Ala Glu Ile Arg Thr Val Cys Glu Arg Ile Asn Asn Glu Leu
189                 350                 355                 360
190
191   GGA AGC CCG GGA TAC CAG CCC GTT GTG TTA ATT GAT GGG CCC GTT TCG      1155
192   Gly Ser Pro Gly Tyr Gln Pro Val Val Leu Ile Asp Gly Pro Val Ser
193           365                 370                 375
194
195   TTA AGT GAA AAA GCT GCT TAT TAT GCT ATC GCC GAT ATG GCA ATT GTT      1203
196   Leu Ser Glu Lys Ala Ala Tyr Tyr Ala Ile Ala Asp Met Ala Ile Val
197           380                 385                 390
198
199   ACA CCG TTA CGT GAC GGA CTG AAT CTT ATC CCG TAC GAG TAC GTC GTT      1251
200   Thr Pro Leu Arg Asp Gly Leu Asn Leu Ile Pro Tyr Glu Tyr Val Val
201       395                 400                 405
202
203   TCC CGA CAA AGT GTT AAT GAC CCA AAT CCC AAT ACT CCA AAA AAG AGC      1299
204   Ser Arg Gln Ser Val Asn Asp Pro Asn Pro Asn Thr Pro Lys Lys Ser
205   410                 415                 420                 425
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206
207  ATG CTA GTG GTC TCC GAG TTC ATC GGT GTT TCA CTA TCT TTA ACC GGG      1347
208  Met Leu Val Val Ser Glu Phe Ile Gly Val Ser Leu Ser Leu Thr Gly
209                  430                 435                 440
210
211  GCC ATA CGG GTC AAC CCA TGG GAT GAG TTG GAG ACA GCA GAA GCA TTA      1395
212  Ala Ile Arg Val Asn Pro Trp Asp Glu Leu Glu Thr Ala Glu Ala Leu
213              445                 450                 455
214
215  TAC GAC GCA CTC ATG GCT CCT GAT GAC CAT AAA GAA ACC GCC CAC ATG      1443
216  Tyr Asp Ala Leu Met Ala Pro Asp Asp His Lys Glu Thr Ala His Met
217          460                 465                 470
218
219  AAA CAG TAT CAA TAC ATT ATC TCC CAT GAT GTA GCT AAC TGG GCT AGC      1491
220  Lys Gln Tyr Gln Tyr Ile Ile Ser His Asp Val Ala Asn Trp Ala Ser
221      475                 480                 485
222
223  TTC TTT CAA GAT TTA GAG CAA GCG TGC ATC GAT CAT TCT CGT AAA CGA      1539
224  Phe Phe Gln Asp Leu Glu Gln Ala Cys Ile Asp His Ser Arg Lys Arg
225  490                 495                 500                 505
226
227  TGC ATG AAT TTA GGA TTT GGG TTA GAT ACT AGA GTC GTC TTT TTG ATG      1587
228  Cys Met Asn Leu Gly Phe Gly Leu Asp Thr Arg Val Val Phe Leu Met
229                  510                 515                 520
230
231  AGA AGT TTA GCA AGT TGG ATA AAG ATG TCT TGG AAG AAT GCT TAT TCC      1635
232  Arg Ser Leu Ala Ser Trp Ile Lys Met Ser Trp Lys Asn Ala Tyr Ser
233              525                 530                 535
234
235  ATG GCT CAA AAT CGG GCC ATA CTT TTG GAC TAT GAC GGC ACT GTT ACT      1683
236  Met Ala Gln Asn Arg Ala Ile Leu Leu Asp Tyr Asp Gly Thr Val Thr
237          540                 545                 550
238
239  CCA TCT ATC AGT AAA TCT CCA ACT GAA GCT GTT ATC TCC ATG ATC AAC      1731
240  Pro Ser Ile Ser Lys Ser Pro Thr Glu Ala Val Ile Ser Met Ile Asn
241      555                 560                 565
242
243  AAA CTG TGC AAT GAT CCA AAG AAC ATG GTG TTC ATC GTT AGT GGA CGC      1779
244  Lys Leu Cys Asn Asp Pro Lys Asn Met Val Phe Ile Val Ser Gly Arg
245  570                 575                 580                 585
246
247  AGT AGA GAG AAA ATC TTG GCA GTT GGT TCG GCG CGT GTG AGA ACC CGC      1827
248  Ser Arg Glu Lys Ile Leu Ala Val Gly Ser Ala Arg Val Arg Thr Arg
249                  590                 595                 600
250
251  CAT TGC ACT GAG CAC GGA TAC TTT ATA AGG TGG GCG GGT GAT CAA GAA      1875
252  His Cys Thr Glu His Gly Tyr Phe Ile Arg Trp Ala Gly Asp Gln Glu
253              605                 610                 615
254
255  TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG ATG GAT GGA AAT      1923
256  Trp Glu Thr Cys Ala Arg Glu Asn Asn Val Gly Trp Met Asp Gly Asn
257          620                 625                 630
258
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/779,460B*

DATE: 04/13/98
TIME: 14:27:54

INPUT SET: S24825.raw

Line	Error	Original Text
47	Wrong Classification	(C) CLASSIFICATION: 435